AMENDMENT TO THE CLAIMS

LISTING OF CLAIMS:

Claims 1-74 (cancelled)

Claim 75. (new) A crystallized complex of KSP and a ligand thereof, wherein the relative structural coordinates of the amino acid residues of KSP are selected from the group set forth in one of the following:

a) Table 1 ± the root mean square deviation from the conserved backbone atoms of not more than about 2 Å;

b) Table 2 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 2 Å;

c) Table 3 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 2 Å; and

d) Table 4 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 2 Å.

Claim 76. (new) The crystallized complex of Claim 75, wherein the relative structural coordinates of the amino acid residues are as set forth in Table 1 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 0.5 Å.

Claim 77. (new) The crystallized complex of Claim 75 wherein said ligand binds said KSP at a ligand binding site comprising the KSP amino acid residues 115 (M), 116(E), 117(G), 118(E), 119(R), 127(W), 130(D), 132(L), 133(A), 134(G), 136(I), 137(P), 160(L) 211(Y), 214(L), 215(E), 217(G), 218(A), 221(R) and 239(F).

Claim 78. (new) The crystallized complex of Claim 75, wherein the relative structural coordinates of the amino acid residues are as set forth in Table 2 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 0.5 Å.

Claim 79. (new) The crystallized complex of Claim 75, wherein said ligand binds said KSP at a ligand binding site comprising the KSP amino acid residues 115 (M), 116(E), 117(G), 118(E), 119(R), 127(W), 130(D),

132(L), 133(A), 134(G), 136(I), 137(P), 160(L) 211(Y), 214(L), 215(E), 217(G), 218(A), 221(R) and 239(F).

Claim 80. (new) The crystallized complex of Claim 75, wherein the relative structural coordinates of the amino acid residues are as set forth in Table 3 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 0.5 Å.

Claim 81. (new) The crystallized complex of Claim 75, wherein said ligand binds said KSP at a ligand binding site comprising the KSP amino acid residues 115 (M), 116(E), 117(G), 118(E), 119(R), 127(W), 130(D), 132(L), 133(A), 134(G), 136(I), 137(P), 160(L) 211(Y), 214(L), 215(E), 217(G), 218(A), 221(R) and 239(F).

Claim 82. (new) The crystallized complex of Claim 75, wherein the relative structural coordinates of the amino acid residues are as set forth in Table 4 ± the root mean square deviation from the conserved backbone atoms of said amino acids of not more than about 0.5 Å.

Claim 83. (new) The crystallized complex of Claim 75, wherein said ligand binds said KSP at a ligand binding site comprising the KSP amino acid residues 115 (M), 116(E), 117(G), 118(E), 119(R), 127(W), 130(D), 132(L), 133(A), 134(G), 136(I), 137(P), 160(L) 211(Y), 214(L), 215(E), 217(G), 218(A), 221(R) and 239(F).

Claim 84. (new) A ligand binding site of a KSP protein comprising the relative structural coordinates set forth in Table 5 ± the root mean square deviation from the backbone atoms of said amino acids is not more than about 2 Å.

Claim 85. (new) The ligand binding site of a KSP protein according to Claim 84 comprising the relative structural coordinates set forth in Table 5 ± the root mean square deviation from the backbone atoms of said amino acids is not more than about 0.5 Å.

Claim 86. (new) The ligand binding site of a KSP protein according to Claim 84 comprising the relative structural coordinates of the KSP amino acid residues 115 (M), 116(E), 117(G), 118(E), 119(R), 127(W), 130(D), 132(L), 133(A), 134(G), 136(I), 137(P), 160(L) 211(Y), 214(L), 215(E), 217(G), 218(A), 221(R) and 239(F) as set forth in a table selected from a group consisting of Tables 1, 2, 3 and 4, ± the root mean square deviation from the backbone atoms of said amino acids is not more than about 2 Å.

Claim 87. (new) A method for identifying an agent that interacts with a ligand binding site of human KSP, comprising the steps of:

(a) determining a ligand binding site of KSP from a three-dimensional model of the KSP binding site as set forth in Table 5, ± the root mean square deviation from the backbone atoms of said amino acids of not more than about 2.0 Å; and

(b) performing computer fitting analysis to identify an agent which interacts with said ligand binding site.

Claim 88. (new) A method for identifying a potential inhibitor of KSP function, comprising the steps of:

(a) generating a three-dimensional model of KSP using the relative structural coordinates as set forth in a table selected from Tables 1, 2, 3 and 4, ± a root mean square deviation from the backbone atoms of said amino acids of not more than about 2.0 Å;

(b) employing said three-dimensional model to design or select a potential inhibitor; and

(c) synthesizing or obtaining said potential inhibitor.

Claim 89. (new) The method according to Claim 88 wherein the potential inhibitor is designed *de novo*.

Claim 90. (new) The method of Claim 88, further comprising the steps of:

(a) contacting said potential inhibitor with KSP in the presence of a KSP binding molecule, and

(b) determining the effect the potential inhibitor has on binding between KSP and the KSP binding molecule.

Claim 91. (new) A machine-readable data storage medium, comprising a data storage material encoded with machine readable data which, when using a machine programmed with instructions for using said data, is capable of displaying a graphical three-dimensional representation of a molecular complex of a compound bound to the ligand binding site of human KSP, said three-dimensional representation comprising the structural coordinates of the KSP as set forth in a table selected from Tables 1-4 or a homologue of said molecular complex, wherein said homologue comprises a binding site that has a root mean square deviation from the backbone atoms of said KSP of not more than about 2.0 Å.

Claim 92. (new) A method for determining the three-dimensional structure of a complex of KSP with a ligand thereof, which comprises obtaining X-ray diffraction data for crystals of the complex comprising the ligand bound to KSP at a ligand binding site; and utilizing said data to define the three-dimensional structure of the complex.

Claim 93. (new) A method of identifying an inhibitor of KSP wherein the inhibitor binds to the ligand binding site according to Claim 84 which comprises determining the shift in the fluorescence of an amino acid residue at position 127 of KSP, wherein said amino acid residue is tryptophan.

Claim 94. (new) The method according to Claim 93 which comprises the steps of:

(a) contacting KSP with the test compound and a nucleotide and measuring the fluorescence of the mixture at the peak emission wavelength for W127 in KSP;

(b) contacting KSP with a nucleotide and measuring the fluorescence of the mixture at the peak emission wavelength for W127 in KSP; and

(c) comparing the fluorescence of the mixture of KSP, the test compound and the nucleotide with the fluorescence of the mixture of KSP with the nucleotide alone.